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 (REV. 10-96)

U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

 ATTORNEY DOCKET NUMBER
 A-64383-2

**TRANSMITTAL LETTER TO THE UNITED STATES
 DESIGNATED/ELECTED OFFICE (DO/EO/US)
 CONCERNING A FILING UNDER 35 U.S.C. 371**

U.S. APPLICATION NO. (If known, sect 37 C.F.R. 1.5)

09/355214
 INTERNATIONAL APPLICATION NO.
 PCT/US98/01394

 INTERNATIONAL FILING DATE
 23 January 1998 (23.01.98)

 PRIORITY DATE CLAIMED
 24 January 1997 (24.01.97)

TITLE OF INVENTION

BLNK PROTEINS

APPLICANT(S) FOR DO/EO/US

CHAN, Andrew C. and FU, Chong

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a FIRST submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371
3. ☒ This is an express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
 - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☒ has been transmitted by the International Bureau. (see enclosed Form PCT/IB/308)
 - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US)
6. ☐ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☒ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11. to 16. below concern other document(s) or information included:

11. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
12. ☒ An assignment document for recording (Andrew Chan to Washington University). A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
 - ☒ An assignment document for recording (Chong Fu to Washington University). A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13. ☐ A FIRST preliminary amendment.
 - ☐ A SECOND or SUBSEQUENT preliminary amendment.
14. ☐ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☒ Other items or information.
 - Power of Attorney by Assignee
 - Verified Statement Claiming Small Entity Status

510 Rec'd PCT/PTO 23 JUL 1999

U.S. APPLICATION NO. (If known, see 37 C.F.R. 1.53)

INTERNATIONAL APPLICATION NO.

ATTORNEY'S DOCKET NUMBER

09/355214

PCT/US98/01394

A-64383-2

17. ☒ The following fees are submitted:**Basic National Fee (37 CFR 1.492(a)(1)-(5)):**

Search Report has been prepared by the EPO or JPO \$840.00

International preliminary examination fee paid to USPTO (37 CFR 1.482)
..... \$670.00No international preliminary examination fee paid to USPTO (37 CFR 1.482)
but international search fee paid to USPTO (37 CFR 1.445(a)(2)) \$760.00Neither international preliminary examination fee (37 CFR 1.482) nor international search
fee (37 CFR 1.445(a)(2)) paid to USPTO \$970.00International preliminary examination fee paid to USPTO (37 CFR 1.482)
and all claims satisfied provisions of PCT Article 33(2)-(4) \$96.00**ENTER APPROPRIATE BASIC FEE AMOUNT =****CALCULATIONS** PTO USE ONLY

\$ 840.00

Surcharge of \$130.00 for furnishing the oath or declaration later than ☐ 20 ☐ 30
months from the earliest claimed priority date (37 CFR 1.492(e)).

\$

CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE
Total Claims	22	-20 =	2
Independent Claims	9	-3 =	6
Multiple dependent claims (if applicable)			

X \$ 18.00

\$ 18.00

X \$ 78.00

\$ 468.00

+ \$ 260.00

\$

TOTAL OF ABOVE CALCULATIONS =

\$ 1,326.00

Reduction by 1/2 for filing by small entity, if applicable. Verified Small x
Entity statement must also be filed. (Note 37 CFR 1.9, 1.27, 1.28).

\$ 663.00

SUBTOTAL =

\$ 663.00

Processing fee of \$130.00 for furnishing the English translation later than ☐ 20 ☐ 30
months from the earliest claimed priority date (37 CFR 1.492(f)).

\$

+

TOTAL NATIONAL FEE =

\$ 663.00

Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be
accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property

\$ 80.00

+

TOTAL FEES ENCLOSED =

743.00

Amount to be:
refunded \$

charged \$

a. ☒ A check in the amount of \$743.00 to cover the above fees is enclosed.b. ☐ Please charge my Deposit Account No. 06-1300 in the amount of \$ to cover the above
fees.c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment
to Deposit Account No. 06-1300 (Order No. A-64383-2/RFT)**NOTE:** Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted
to restore the application to pending status.

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REGISTRATION NUMBER

Applicant or Patentee: Andrew C. Chan, et al. Att's Docket No.: A-64383-2/RFT/RMS
 Serial or Patent No.: _____ Filed or Issued: Herewith
 For: BLNK PROTEINS

**VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY
 STATUS (37 CFR 1.9(f) and 1.27(d)) - NONPROFIT ORGANIZATION**

I hereby declare that I am an official empowered to act on behalf of the nonprofit organization identified below:

NAME OF ORGANIZATION Washington University

ADDRESS OF ORGANIZATION One Brookings Drive, St. Louis, MO 6313

TYPE OF ORGANIZATION

- ☒ UNIVERSITY OR OTHER INSTITUTION OF HIGHER EDUCATION
☐ TAX EXEMPT UNDER INTERNAL REVENUE SERVICE CODE (26 USC 501(a) and 501(c)(3))
☐ NONPROFIT SCIENTIFIC OR EDUCATIONAL UNDER STATUTE OF STATE OF THE UNITED STATES OF AMERICA
 (NAME OF STATE _____) (CITATION OF STATUTE _____)
☐ WOULD QUALIFY AS NONPROFIT SCIENTIFIC OR EDUCATIONAL UNDER STATUTE OF STATE OF THE UNITED STATES OF AMERICA IF LOCATED IN THE UNITED STATES OF AMERICA
 (NAME OF STATE _____) (CITATION OF STATUTE _____)

I hereby declare that the nonprofit organization identified above qualifies as a nonprofit organization as defined in 37 CFR 1.9(e) for purposes of paying reduced fees under Section 41(a) or (b) of Title 35, United States Code, with regard to the invention entitled BLNK Proteins by inventor(s) Andrew C. Chan and Chong Fu described in

☒ the specification filed herewith

☐ application serial no. _____, filed _____

I hereby declare that rights under contract or law have been conveyed to and remain with the nonprofit organization having rights to the invention as listed below* and no rights to the invention are held by any person, other than the inventor, who could not qualify as a small business concern under 37 CFR 1.9(d) or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e). *NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27)

NAME: Howard Hughes Medical Institute

ADDRESS: 4000 Jones Bridge Road, Chevy Chase, Maryland 20815-6789

☐ Individual ☐ Small Business Concern ☒ Nonprofit Organization

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 CFR 1.28(b)).

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

NAME OF PERSON SIGNING Andrew Neighbour, Ph.D.

TITLE IN ORGANIZATION Director, Technology Management

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St. Louis, MO 63110

SIGNATURE P. Neighbour
 Form 1.25

DATE 7/21/99

BLNK PROTEINS

This application is a continuing application of U.S.S.N.s 08/819,013, filed March 17, 1997, and 08/788,322, filed January 24, 1997.

FIELD OF THE INVENTION

The invention relates to novel BLNK proteins, nucleic acids and antibodies.

BACKGROUND OF THE INVENTION

B cell function is dependent upon the ability of the membrane B cell antigen receptor (BCR) to bind antigen and to effectively induce an efficient cascade of biochemical events from the membrane to the nucleus. These events culminate in the cytosol to rearrange the morphology of the cell through cytoskeletal reorganization and in the nucleus to activate the transcription of new genes to promote cellular differentiation and proliferation. These biochemical and cellular events are required for the ability of B cells to mature and function to produce an efficient immune response to foreign pathogens. Conversely, aberrant activation of B cells can lead to unregulated cellular proliferation and uncontrolled clonal expansion, resulting in B cell tumors. In addition, unregulated activation of B cells may also contribute to a variety of autoimmune diseases mediated by self-reactive antibodies. Thus, the ability to modulate BCR mediated signaling events may provide a rational approach in the treatment of B-cell mediated tumors and also in autoimmune diseases in which aberrant B cell activation may occur.

Ligand binding of the BCR to antigen activates at least two major distinct biochemical pathways within the cell. The first results in increases in intracellular calcium levels that is mediated by an enzyme known as γ isoform of phospholipase C (PLC- γ). Two forms of PLC- γ , γ -1 and γ -2, appear to be capable of mediating this calcium response. The second major biochemical pathway activated through antigen engagement of the BCR is the activation of the ras pathway. Activation of this pathway appears to be mediated by a molecule known as Grb2. Grb2 is an adapter molecule containing two SH3 domains that mediate its interaction with the guanine nucleotide exchange factor, Son of Sevenless (SoS) which in turn activates the ras pathway by facilitating the exchange of GDP for GTP on the ras molecule. Activation of both the ras and calcium pathways are required for efficient BCR function. The molecular mechanisms by which Grb2 and PLC- γ become activated by the BCR remain unclear at this time.

A third, though less characterized pathway, activated by the BCR is cytoskeletal rearrangement and aggregation of the BCR (a phenomenon known as capping). The molecular mechanisms of this pathway are unclear.

While the biochemical mechanisms by which the calcium and ras signaling pathways become activated remain unclear, studies have demonstrated that both of these pathways require the activation at least two families of protein tyrosine kinases (PTKs). The first family is the Src-family of PTKs which can associate with the BCR. A second family is the Syk PTK which interacts with activated, phosphorylated BCR. Abrogation of the function of either Src-PTKs or Syk interferes with calcium and ras signaling pathways and results in a non-functional BCR.

Thus, the discovery of molecules which interact with either Grb2, PLC- γ or Syk, and thus play a role in the regulation of the ras and calcium signaling pathways, are desired. Accordingly, it is an object of the present invention to provide such molecules, termed "BLNK" proteins, and to provide methods of using such molecules in screening assays.

SUMMARY OF THE INVENTION

In accordance with the objects outlined above, the present invention provides recombinant nucleic acids encoding BLNK proteins, and expression vectors and host cells containing the BLNK nucleic acids.

In an additional aspect, the present invention provides methods of producing a BLNK protein comprising culturing a host cell transformed with nucleic acid encoding a BLNK protein; and expressing the nucleic acid to produce a BLNK protein.

In a further aspect, the present invention provides recombinant BLNK proteins and pharmaceutical compositions comprising BLNK proteins.

In an additional aspect, the present invention provides antibodies which bind BLNK proteins.

In a further aspect, the present invention provides methods for detecting a BLNK protein in a target sample. The methods comprise contacting a labelled polypeptide that binds a BLNK protein with the target sample and assaying for the presence of binding between the labelled polypeptide and BLNK, if present.

In an additional aspect the present invention provides methods for screening for a bioactive agent capable of inhibiting the bioactivity of a BLNK protein. The method comprise combining a BLNK protein and a candidate bioactive agent, and determining the binding of said candidate agent to BLNK protein.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 depicts the amino acid sequence of human BLNK 1.

Figure 2 depicts the nucleic acid sequence of human BLNK 1.

Figure 3 depicts the amino acid sequence of human BLNK 2.

Figure 4 depicts the nucleic acid sequence of human BLNK 2.

Figure 5 depicts the amino acid sequence of mouse BLNK 1. The human cDNA was used to screen a mouse cDNA library. A full length mouse cDNA encoding BLNK-1 was isolated and sequenced. It demonstrates significant amino acid identity (88%) with human BLNK-1. The mouse only demonstrates a single gene product that corresponds to the full length human BLNK-1.

Figure 6 depicts the nucleic acid sequence of mouse BLNK 1.

Figure 7 depicts a schematic diagram of the BLNK proteins.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides novel BLNK proteins. In a preferred embodiment, the BLNK proteins are from vertebrates, more preferably from mammals, and in the preferred embodiment, from rats, mice, primates, or humans. However, using the techniques outlined below, BLNK proteins from other organisms may also be obtained.

Without being bound by theory, it appears that there are a number of related BLNK proteins and nucleic acids. For example, in the human, it appears that there are at least two separate BLNK proteins, BLNK 1 and BLNK 2, that result from differential splicing of a single nucleic acid. BLNK-2 is the result of an excision of a 23 amino acid exon from BLNK-1. Both forms are expressed in normal human B cells. In the mouse, there is only one BLNK protein which corresponds to the full length (BLNK 1) protein in humans. These BLNKs share basic homology to each other, and a general lack of homology to any other known proteins or nucleic acids.

Thus, a BLNK protein of the present invention may be identified in several ways. A BLNK nucleic acid or BLNK protein is initially identified by substantial nucleic acid and/or amino acid sequence homology to the sequences shown in Figures 1, 2, 3, 4, 5 or 6. Such homology can be based upon the overall nucleic acid or amino acid sequence.

As used herein, a protein is a "BLNK protein" if the overall homology of the protein sequence to the amino acid sequences shown in Figures 1, 3 or 5 is preferably greater than about 40%, more preferably greater than about 50% and most preferably greater than 75-80%. In some embodiments the homology will be as high as about 90 to 95 or 98%. This homology will be determined using standard techniques known in the art, such as the Best Fit sequence program described by Devereux *et al.*, *Nucl. Acid Res.* 12:387-395 (1984) or the BLASTX program (Altschul *et al.*, *J. Mol. Biol.* 215, 403-410). The alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer amino acids than the proteins shown in the Figures, it is understood that the percentage of homology will be determined based on the number of homologous amino acids in relation to the total number of amino acids. Thus, for example, homology of sequences shorter than that shown in the Figures, as discussed below, will be determined using the number of amino acids in the shorter sequence.

BLNK-1 has limited homology to SLP-76, an SH2 containing leukocyte protein of 76,000 MW. SLP-76 is a protein that undergoes tyrosine phosphorylation following activation of the T cell antigen receptor (TCR). SLP-76 was cloned (see Jackman *et al.*, *J. Biol. Chem.* 270:7029-7032 (1995)) as a tyrosine phosphorylated molecule that interacts with Grb2 and PLC- γ -1. Similar to BLNK-1, SLP-76 also has the three structural regions depicted in Figure 7. The tyrosine phosphorylation of SLP-76 is required for TCR mediated cytokine secretion. The overall homology between SLP-76 and BLNK-1 is 33% identity.

As discussed above, BLNK proteins include BLNK 1 and BLNK 2 proteins. BLNK proteins may be identified in one aspect by significant homology to at least one and preferably all of the regions schematically shown in Figure 7, including the acidic region (residues 51-109),

the proline rich region in the central portion of the molecule (130-345), putatively identified as a binding site for SH-3 containing proteins, and an SH2 domain at the C-terminus (346-438).

5 The N-terminal region of BLNK protein contains an acidic region (amino acids 51-109). The amino acid consensus sequence of this area is rather loose, and consists basically of three YEXP sequences preceeded by a negatively charged amino acid (D or E) in the -2 position. The consensus sequence is D/EXYEXPX D/EXYXXPXD/EX YEPP.

10 This acidic region contains tyrosine phosphorylation sites at (human BLNK-1 numbering) Tyr 71, Tyr83, Tyr95, Tyr177, and Tyr187. Biochemical and genetic approaches have confirmed that all of these tyrosines are phosphorylated following B-cell activation, and that it is the Syk protein tyrosine kinase that is responsible for phosphorylating BLNK following B cell activation. Syk can phosphorylate BLNK when co-expressed in insect cells, and in
15 vitro. BLNK is not phosphorylated in cells lacking Syk.

20 The central portion of BLNK proteins contain a proline rich region, amino acids 130-345, which serves as the binding site for SH3 containing proteins. This site has been implicated as the binding site for Grb2.

The C-terminus of BLNK proteins contains an SH2 domain, amino acids 346-438, which may bind tyrosine phosphorylated proteins. SH2 domains are known to be involved in binding of signal pathway proteins.

25 BLNK proteins of the present invention may be shorter or longer than the amino acid sequences shown in the Figures. Thus, in a preferred embodiment, included within the definition of BLNK proteins are portions or fragments of the sequences shown in Figures 1, 2, 3, 4, 5 and 6. Alternatively, longer fragments of BLNK proteins can be made.

BLNK proteins may also be identified as being encoded by BLNK nucleic acids. Thus, BLNK proteins are encoded by nucleic acids that will hybridize to the sequences depicted in Figures 2, 4 and 6, as outlined herein. In a preferred embodiment, high stringency conditions are used, as are known in the art.

5 In a preferred embodiment, when the BLNK protein is to be used to generate antibodies, the BLNK protein must share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is meant a portion of a protein which will generate and/or bind an antibody. Thus, in most instances, antibodies made to a smaller BLNK protein will be able to bind to the full length protein. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. The BLNK antibodies of the invention specifically bind to BLNK proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a binding constant in the range of at least 10^4 - 10^6 M^{-1} , with a preferred range being 10^7 - 10^9 M^{-1} . The antibodies may be either polyclonal or monoclonal, with monoclonal antibodies being preferred.

10 In the case of the nucleic acid, the overall homology of the nucleic acid sequence is commensurate with amino acid homology but takes into account the degeneracy in the genetic code and codon bias of different organisms. Accordingly, the nucleic acid sequence homology may be either lower or higher than that of the protein sequence. Thus the homology of the nucleic acid sequence as compared to the nucleic acid sequence of Figures 2, 4 or 6 is preferably greater than 40%, more preferably greater than about 45%, particularly greater than about 50% and most preferably greater than 55%. In some embodiments the homology will be as high as about 70, 80, 90, 95 or 98%.

20 25 In a preferred embodiment, a BLNK nucleic acid encodes a BLNK protein; BLNK 1 nucleic acids encode BLNK 1 proteins, and BLNK 2 nucleic acids encode BLNK 2 proteins. As will be appreciated by those in the art, due to the degeneracy of the genetic code, an extremely large number of nucleic acids may be made, all of which encode the BLNK proteins of the present invention. Thus, having identified a particular amino acid sequence, those skilled in

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the art could make any number of different nucleic acids, by simply modifying the sequence of one or more codons in a way which does not change the amino acid sequence of the BLNK.

5 In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, for example, nucleic acids which hybridize under high stringency to the nucleic acid sequences shown in Figures 2, 4 or 6 or their complements are considered BLNK genes. High stringency conditions are known in the art; see for example Maniatis et al., Molecular Cloning: A Laboratory Manual, 2d Edition, 1989, and Short Protocols in Molecular Biology, ed. Ausubel, et al., both of which are hereby incorporated by reference.

10 In another embodiment, less stringent hybridization conditions are used; for example, moderate or low stringency conditions may be used, as are known in the art; see Maniatis and Ausubel, supra.

15 The BLNK proteins and nucleic acids of the present invention are preferably recombinant. As used herein, "nucleic acid" may refer to either DNA or RNA, or molecules which contain both deoxy- and ribonucleotides. The nucleic acids include genomic DNA, cDNA and oligonucleotides including sense and anti-sense nucleic acids. Such nucleic acids may also
20 contain modifications in the ribose-phosphate backbone to increase stability and half life of such molecules in physiological environments.

25 The nucleic acid may be double stranded, single stranded, or contain portions of both double stranded or single stranded sequence. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid by endonucleases, in a form not normally found in nature. Thus an isolated BLNK nucleic acid, in a linear form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or
30 organism, it will replicate non-recombinantly, i.e. using the in vivo cellular machinery of the

host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

5 Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e. through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. For example, the protein may be isolated or purified away from some or all of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. For example, an isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a BLNK protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of a inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

Also included with the definition of BLNK protein are other BLNK proteins of the BLNK family, and BLNK proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related BLNK proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the BLNK nucleic acid sequence. Thus, useful probe or primer sequences may be designed to all or part of the acidic region. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length,

with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art.

Once the BLNK nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire BLNK protein nucleic acid. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant BLNK nucleic acid can be further used as a probe to identify and isolate other BLNK nucleic acids. It can also be used as a "precursor" nucleic acid to make modified or variant BLNK nucleic acids and proteins.

Using the nucleic acids of the present invention which encode a BLNK protein, a variety of expression vectors are made. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the BLNK protein. "Operably linked" in this context means that the transcriptional and translational regulatory DNA is positioned relative to the coding sequence of the BLNK protein in such a manner that transcription is initiated. Generally, this will mean that the promoter and transcriptional initiation or start sequences are positioned 5' to the BLNK protein coding region. The transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the BLNK protein; for example, transcriptional and translational regulatory nucleic acid sequences from *Bacillus* are preferably used to express the BLNK protein in *Bacillus*. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, the transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

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In addition, the expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art.

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In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The BLNK proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a BLNK protein, under the appropriate conditions to induce or cause expression of the BLNK protein. The conditions appropriate for BLNK protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

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Appropriate host cells include yeast, bacteria, archebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Drosophila melangaster* cells, *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, SF9 cells, C129 cells, 293 cells, Neurospora, BHK, CHO, COS, and HeLa cells, fibroblasts, Schwannoma cell lines, and immortalized mammalian myeloid, lymphoid cell lines, and insect Hi5 cells.

In a preferred embodiment, the BLNK proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art. A mammalian promoter is any DNA sequence capable of binding mammalian RNA polymerase and initiating the downstream (3') transcription of a coding sequence for BLNK protein into mRNA. A promoter will have a transcription initiating region, which is usually placed proximal to the 5' end of the coding sequence, and a TATA box, usually located 25-30 base pairs upstream of the transcription initiation site. The TATA box is thought to direct RNA polymerase II to begin RNA synthesis at the correct site. A mammalian promoter will also contain an upstream promoter element (enhancer element), typically located within 100 to 200 base pairs upstream of the TATA box. An upstream promoter element determines the rate at which transcription is initiated and can act in either orientation. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter.

Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. The 3' terminus of the mature mRNA is formed by site-specific post-translational cleavage and polyadenylation. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, direct microinjection of the DNA into nuclei, etc.

In a preferred embodiment, BLNK proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art.

A suitable bacterial promoter is any nucleic acid sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of the coding sequence of BLNK protein into mRNA. A bacterial promoter has a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region typically includes an RNA polymerase binding site and a transcription initiation site. Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose and maltose, and sequences derived from biosynthetic enzymes such as tryptophan. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; for example, the *tac* promoter is a hybrid of the *trp* and *lac* promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription.

In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. In *E. coli*, the ribosome binding site is called the Shine-Delgarno (SD) sequence and includes an initiation codon and a sequence 3-9 nucleotides in length located 3 - 11 nucleotides upstream of the initiation codon.

The expression vector may also include a signal peptide sequence that provides for secretion of the BLNK protein in bacteria. The signal sequence typically encodes a signal peptide

comprised of hydrophobic amino acids which direct the secretion of the protein from the cell, as is well known in the art. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria).

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The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways.

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These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others.

The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

20 In one embodiment, BLNK proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

25 In a preferred embodiment, BLNK protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*. Preferred promoter sequences for expression in yeast include the inducible GAL1,10 promoter, the promoters from alcohol dehydrogenase, enolase,
30 glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphate-dehydrogenase,

hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, pyruvate kinase, and the acid phosphatase gene. Yeast selectable markers include ADE2, HIS4, LEU2, TRP1, and ALG7, which confers resistance to tunicamycin; the neomycin phosphotransferase gene, which confers resistance to G418; and the CUP1 gene, which allows yeast to grow in the presence of copper ions.

The BLNK protein may also be made as a fusion protein, using techniques well known in the art. Thus, for example, for the creation of monoclonal antibodies, if the desired epitope is small, the BLNK protein may be fused to a carrier protein to form an immunogen. For example, two fusion proteins have been generated to make antibodies; amino acids 4-205 and amino acids 324-457 of human BLNK-1 have each been fused to glutathione-S-transferase, the fusion proteins produced in bacteria and used as immunogens in rabbits (polyclonal antibodies) and mice (monoclonal antibodies). The rabbit polyclonal antibodies immunoprecipitate and immunoblot both human and mouse BLNK-1 (data not shown), and the mouse monoclonal antibodies immunoprecipitate and immunoblot only human BLNK-1 (data not shown). Alternatively, the BLNK protein may be made as a fusion protein to increase expression, or to include an epitope tag or purification tag (i.e. His₆) to allow purification, or for other reasons.

Also included within the definition of BLNK proteins of the present invention are amino acid sequence variants. These variants fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the BLNK protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant BLNK protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the BLNK protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring

analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed BLNK variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of BLNK protein activities; for example, for binding domain mutations, competitive binding studies such as are outlined in the Examples may be done.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger. For example, preferred deletion variants include the deletion of one or more of the three domains, i.e. the acidic domain, the proline rich region, or the SH2 domain.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the BLNK protein are desired, substitutions are generally made in accordance with the following chart:

Chart I

<u>Original Residue</u>	<u>Exemplary Substitutions</u>
Ala	Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro
His	Asn, Gln
Ile	Leu, Val
Leu	Ile, Val
Lys	Arg, Gln, Glu
Met	Leu, Ile
Phe	Met, Leu, Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp, Phe
Val	Ile, Leu

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those shown in Chart I. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g. seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analogue, although variants also are selected to modify the characteristics of the BLNK proteins as needed. Alternatively, the variant may be designed such that the biological activity of the BLNK protein is altered. For example, any or all of the three domains may be altered, i.e. the acidic domain, the proline rich region, or the SH2 domain. For example, one or more of the tyrosine phosphorylation sites may be altered; as outlined herein, a mutant human BLNK-1 has been made which replaces all five of the tyrosine phosphorylation sites with phenylalanine has been done.

In one embodiment, the BLNK nucleic acids, proteins and antibodies of the invention are labelled. By "labelled" herein is meant that a compound has at least one element, isotope or chemical compound attached to enable the detection of the compound. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies or antigens; and c) colored or fluorescent dyes. The labels may be incorporated into the compound at any position.

In a preferred embodiment, the BLNK protein is purified or isolated after expression. BLNK proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the BLNK protein may be purified using a standard anti-BLNK antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, R., Protein Purification, Springer-Verlag, NY (1982). The degree of purification necessary will vary depending on the use of the BLNK protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the BLNK proteins are useful in a number of applications.

BLNK appears to be involved in B cell function in several ways. BLNK is able to interact with phospholipase C, an enzyme that can hydrolyze and activate inositol phospholipids to increase free cytoplasmic calcium levels. Overexpression of wild-type BLNK can increase tyrosine phosphorylation of BLNK and result in additional increases in free cytoplasmic calcium levels. Conversely, expression of a mutant BLNK in which the tyrosine residues that are phosphorylated are substituted with phenylalanine (and thus are unable to be phosphorylated) will decrease calcium levels following B cell activation. Accordingly, one of BLNK's functions is to modulate the ability of the B cell receptor to regulate calcium levels in the cell.

In addition, BLNK has been shown to interact with a variety of proteins in B cells. In addition to Grb2 and PLC, BLNK also interacts with the nck adaptor protein and the Vav protooncogene following BCR activation. Preliminary data (not shown) suggests that these two interactions likely control the ability of B cells to regulate actin polymerization and cytoskeletal reorganization. The cytoskeleton has been demonstrated in other systems to be important in B cell function and in tumor invasiveness, and may serve as a therapeutic target through BLNK to treat B cell related tumors.

As outlined in the examples, Northern blot analysis of BLNK-1 demonstrates that BLNK-1 demonstrates its highest level of expression in spleen/B cells and substantially lower levels of expression, if any, in all other tissues examined. Thus, BLNK-1 has a relatively specific pattern of expression, and thus is highly specific for B-cells. This makes it useful in a number of ways, as there are not many specific B cell markers.

In a preferred embodiment, BLNK proteins and nucleic acids are used in screening assays of candidate bioactive agents that modulate BLNK bioactivity, for potential use to treat B-cell lymphomas. By "modulate" herein is meant that the bioactivity of BLNK is altered, either increased or decreased. In a preferred embodiment, the bioactivity is inhibited. BLNK is putatively critical for the BCR response, and thus for B cell function. Accordingly, BLNK may be used as a target to screen for inhibitors of its function or expression.

In a preferred embodiment, BLNK proteins and nucleic acids are used in screening assays of candidate bioactive agents that modulate BLNK bioactivity, for potential use to treat autoimmune diseases which have hyperactivated B cells.

5 Thus, in a preferred embodiment, the methods comprise screening for a bioactive agent capable of inhibiting the bioactivity of a BLNK protein. By "bioactivity" herein is meant the binding of the BLNK to any of its targets, including Grb2, PLC- γ , the nck adaptor protein and the VAV protooncogene, the regulation of calcium levels, or cytoskeletal organization. That is, bioactive agents that prevent BLNK binding, i.e. interrupt the interaction of BLNK and its target, may be found. The method comprises combining a BLNK protein and a candidate bioactive agent, and determining the binding of the candidate agent to BLNK protein.

10 Generally, in a preferred embodiment of the methods herein, a BLNK polypeptide is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which polypeptides can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include
15 microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the polypeptide is not crucial so long as it is compatible with the reagents and overall methods of
20 the invention, maintains the activity of the peptide and is nondiffusable. Preferred methods of binding include the use of antibodies (which should not hinder the binding of BLNK to its targets, including Grb2, PLC- γ , nck or Vav), direct binding to "sticky" or ionic supports, chemical crosslinking, etc. Following binding of the polypeptide, excess unbound material is removed by washing. The sample receiving areas may then be blocked as needed through
25 incubation with bovine serum albumin (BSA), casein or other innocuous protein.
30

A candidate bioactive agent is added to the assay. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, and the like.

The term "agent" as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., with the capability of directly or indirectly altering the bioactivity of BLNK proteins. Generally a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof.

Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally,

natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means. Known pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification to produce structural analogs.

5 The determination of the binding of the candidate bioactive agent to the BLNK polypeptide may be done in a number of ways. In one embodiment, the candidate bioactive agent is labelled, and binding determined directly.

10 Where the screening assay is a binding assay, one or more of the molecules may be joined to a label, where the label can directly or indirectly provide a detectable signal. Various labels include radioisotopes, fluorescers, chemiluminescers, specific binding molecules, particles, e.g. magnetic particles, and the like. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin etc. For the specific binding members, the
15 complementary member would normally be labeled with a molecule which provides for detection, in accordance with known procedures. In some embodiments, only one of the components is labeled. Alternatively, more than one component may be labeled with different labels; for example, the BLNK polypeptide may be labeled with one fluorophor and the candidate agent labeled with another.

20 In one embodiment, the candidate bioactive agent is labeled. The labeled candidate bioactive agents are added to the BLNK polypeptide for a time sufficient to allow binding, if present. Incubations may be performed at any temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are selected for optimum activity, but may also be
25 optimized to facilitate rapid high through put screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The presence or absence of the labeled component is followed, to indicate binding.

30 In a preferred embodiment, the methods comprise combining a BLNK protein, a candidate bioactive agent, and either Grb2 or PLC- γ , and determining the binding of the BLNK to one

of its targets, including Grb2, PLC- γ , nck or Vav, to determine the effect of the candidate bioactive agent.

Thus, in a preferred embodiment, the methods comprise differential screening to identify bioactive agents that are capable of modulating the bioactivity of BLNK proteins. In this embodiment, the methods comprise combining a BLNK polypeptide and one of BLNK's binding partners, including Grb2, PLC- γ , nck, or Vav, in a first sample. A second sample comprises a candidate bioactive agent, BLNK polypeptide and one of BLNK's binding partners. The binding of BLNK to its binding partner is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of modulating the bioactivity of BLNK.

Alternatively, a preferred embodiment utilizes differential screening to identify drug candidates that bind to the native BLNK, but cannot bind to modified BLNK proteins, for example those that have modifications which eliminate or decrease bioactivity of a BLNK protein; for example BLNK proteins that may no longer be phosphorylated, as outlined herein.

Preferably all control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the BLNK proteins and the Grb2 and/or PLC- γ proteins. Following incubation, all samples are washed free of non-specifically bound material and the amount of bound, labeled material determined. For example, where a radiolabel is employed as a label, the samples may be counted in a scintillation counter to determine the amount of labeled compound.

A variety of other reagents may be included in the screening assay. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used.

The mixture of components may be added in any order that provides for the requisite binding.

The following examples serve to more fully describe the manner of using the above-described invention, as well as to set forth the best modes contemplated for carrying out various aspects of the invention. It is understood that these examples in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All references cited herein are incorporated by reference.

EXAMPLES

Cloning and Characterization of BLNK proteins

Using B cell tumor cell lines and normal B cells, two proteins with apparent molecular masses of 68,000, 70,000, and 76,000 that interact with Grb2 and PLC γ 1 following BCR activation were observed. Moreover, these proteins became phosphorylated on tyrosine residues following BCR crosslinking. Using immunodepletion studies, we demonstrated that the 68K and 70K Mr proteins that interacted with Grb2 and PLC γ 1 were in fact the same protein. More recent data has also suggested that the 68K and 70 K Mr proteins also interact with nck following BCR activation. These initial data suggested to us that these proteins may serve as important regulatory proteins to link the BCR and its associated PTKs with these major downstream signaling functions. Given the ability of these proteins to likely link the proximal BCR and its associated PTKs with downstream signaling functions, we have designated the 68,000 Mr protein as BLNK-2 (B cell LINKER PROTEIN) and the 70,000 Mr protein as BLNK-1.

To further characterize these proteins, we undertook a large scale purification scheme of the 68K and 70K Mr proteins from human B cells. We have derived peptide sequences for both of these proteins and have identified a full length cDNA for human BLNK-1 (the 70K Mr protein). The predicted open reading frame of the BLNK-1 cDNA was consistent with the peptides derived from protein sequencing. This novel cDNA is not represented in the GenBank data base (December, 1996). Northern blot analysis of BLNK-1 demonstrates its

highest level of expression in spleen/B cells and substantially lower levels of expression, if any, in all other tissues examined. Thus, BLNK-1 has a relatively specific pattern of expression for B cells.

5 Analysis of PCR products using cDNA from the human Ramos B cell line demonstrated the presence of two gene products. DNA sequencing of these two gene products demonstrated that these two gene products differ by the absence of 23 amino acids from the BLNK-1 open reading frame. Hence, BLNK-2 appears to be an alternatively spliced form of BLNK-1; a 23 amino acid exon of BLNK-1 is excised in BLNK-2. Thus, it is likely that BLNK-1 and 2
10 form a family of proteins that serve to link the BCR with a variety of signaling and adapter proteins (e.g., Grb2, nck, VAV and PLCg1) to mediate B cell activation.

The open reading frame of BLNK-1 contained three intriguing structural regions (Figure 7). The amino (N)-terminus contains an acidic region which has three potential tyrosine residues for phosphorylation. The central portion of the molecule has a proline rich region which may
15 serve as the binding site for SH3 containing proteins. Binding studies suggest that this region likely serves as the binding site for Grb2. Finally, the carboxy-terminal portion of the molecule has an SH2 domain for binding other tyrosine phosphorylated proteins. Homology search of the protein sequence with the GenBank database revealed homology (33% amino
20 acid identity) with the protein, SLP-76 (SH2-containing leukocyte protein of 76,000 Mr).

Protein Purification and Microsequencing: Ramos Burkitt Lymphoma cells (ATCC) were cultured in RPMI-1640 with 10% fetal calf serum. 1.5×10^{10} cells were collected by centrifugation (1000g x 10 min) and washed once with ice-cold phosphate buffered saline
25 (PBS). The cells were then resuspended in 75 ml ice-cold PBS and divided into 50 microcentrifuge tubes (1.5 ml each). 25 ml anti-hIgM (1.2 mg/ml, Jackson Labs) were added to each tube and inverted twice. Cells were incubated with the stimulating antibody for 5-30 minutes on ice, sedimented by flash centrifugation, and resuspended in an equal volume of pre-warmed PBS (37°C) for 1.5 min. Following stimulation, cells were sedimented and lysed
30 in equal volume of lysis buffer (1% NP-40, 10mM Tris-HCl, pH 8.0, 150 mM NaCl) with

protease and phosphatase inhibitors (10 mM NaF, 1 mM sodium orthovanadate, 10 mg/ml phenylmethanesulfonyl- fluoride, 2 mg/ml aprotinin, 1 mg/ml leupeptin, 2 mg/ml pepstatin, 5 mM EDTA, 10 mg/ml soybean trypsin inhibitor). Cell lysates were pooled and cleared by centrifugation (15,000g x 20 min) and the supernatants were further cleared by
5 ultra-centrifugation (100,000g x 40 min). Cleared lysates were passed through a 2 ml column of glutathione S-transferase (GST) immobilized on Glutathione-Sepharose (Pharmacia, 2 mg/ml). The flowthrough from the GST-Sepharose column was then incubated for ~12 hrs with 2 ml of a 50% slurry of a fusion protein consisting of GST and the C-terminal SH2 domain of PLCg1 [designated as GST-PLCg1(C-SH2)] immobilized on
10 Glutathione-Sepharose. Following binding, the GST-PLCg1(C-SH2) beads were transferred to a column, washed twice with 15 ml high salt lysis buffer (lysis buffer with 0.5 mM NaCl), and twice with 15 ml lysis buffer. Beads were transferred to a 15 ml conical tube and washed with 15 ml lysis buffer. Proteins bound to GST-PLCg1(C-SH2) were then eluted twice by incubating the beads with 2 ml lysis buffer containing 1% SDS for 5 min at 95°C and eluants combined (4 ml). Lysis buffer was added to dilute the SDS to 0.1%. The diluted sample was
15 incubated with 1 ml 50% slurry of an anti-phosphotyrosine antibody (PY20) immobilized on Protein A-Sepharose (1 mg/ml) for 5 hrs at 4°C. The beads were then washed with lysis buffer (5 x 10 ml), transferred to 2 microcentrifuge tubes, washed two additional times with low salt buffer A (20 mM Tris-HCl, pH 8.0, 25 mM NaCl), and eluted twice with 500 µl/tube
20 of 100 mM phenylphosphate (Sigma) in buffer A. The eluants were combined (2 ml), adjusted to 0.1% SDS, and dialyzed against buffer A containing 0.1% SDS.

Three similar scale preparations (1.5×10^{10} cells each) were combined and the final sample (6 ml) was concentrated using a Centriplus Concentrator (Amicon). Proteins were resolved on a
25 1.5 mm 7% SDS-polyacrylamide gel and visualized with Coomassie Brilliant Blue R 250 (Biorad). Proteins of interest were excised and subjected to enzymatic digestion. Peptides were resolved by standard biochemical techniques using HPLC and sequenced using automated Edman degradation.

Immobilization of GST-fusion proteins: GST fusion proteins were incubated with Glutathione Sepharose (Pharmacia) in PBS for 30 min at 4°C, washed extensively with PBS, and subsequently incubated at room temperature for 30 minutes with 10 bead-volumes of freshly prepared dimethylpimelimidate (Sigma) in 50mM carbonate buffer, pH 9.2. The beads were then washed once with 0.2 M ethanolamine (pH 8.0) and rotated for 2 hours with 10 bead-volumes of 0.2 M ethanolamine (pH 8.0). Beads were again washed with PBS and stored at 4°C in PBS, 0.1% sodium azide. Immobilization of PY20 on Protein A-Sepharose (Pharmacia) were performed in a similar fashion.

cDNA cloning of BLNK-1: Degenerate oligonucleotides based on peptide sequences were used (TCGAGAATTCAAA/GAAA/GCCACNACNCC from the peptide KKPTTPLK and CTGAGGATCCTTIGTNGCC/TTCG/A/TATA/GAA from KRVYNIPVRFIEATK). Ramos mRNA was used for first strand cDNA synthesis using random primers and the degenerate oligonucleotides used as the 5' and 3' primers. Conditions used for PCR were: 94°C, 1 min, 40°C annealing temperature for 1 min, and 72°C extension temperature for 1 min. These initial conditions were used for 4 cycles. Subsequently, the annealing temperature was raised to 50°C for additional 30 cycles. A 450 nucleotide fragment was observed and used as a probe to screen a human tonsillar B cell library. Positive clones were sequenced using standard dideoxynucleotide sequencing.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Washington University

(ii) TITLE OF INVENTION: BLNK PROTEINS

10 (iii) NUMBER OF SEQUENCES: 12

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(v) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

25 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US98/
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

30 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/819,013
(B) FILING DATE: 17-MAR-1997

(vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US 08/788,322
(B) FILING DATE: 24-JAN-1997

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(2) INFORMATION FOR SEQ ID NO:1:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 456 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
55 (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5	Met	Asp	Lys	Leu	Asn	Lys	Ile	Thr	Val	Pro	Ala	Ser	Gln	Lys	Leu	Arg	1	5	10	15
	Gln	Leu	Gln	Lys	Met	Val	His	Asp	Ile	Lys	Asn	Asn	Glu	Gly	Gly	Ile	20	25	30	
10	Met	Asn	Lys	Ile	Lys	Lys	Leu	Lys	Val	Lys	Ala	Pro	Pro	Ser	Val	Pro	35	40	45	
	Arg	Arg	Asp	Tyr	Ala	Ser	Glu	Ser	Pro	Ala	Asp	Glu	Glu	Glu	Gln	Trp	50	55	60	
	Ser	Asp	Asp	Phe	Asp	Ser	Asp	Tyr	Glu	Asn	Pro	Asp	Glu	His	Ser	Asp	65	70	75	80
20	Ser	Glu	Met	Tyr	Val	Met	Pro	Ala	Glu	Glu	Asn	Ala	Asp	Asp	Ser	Tyr	85	90	95	
	Glu	Pro	Pro	Pro	Val	Glu	Gln	Glu	Thr	Arg	Pro	Val	His	Pro	Ala	Leu	100	105	110	
25	Pro	Phe	Ala	Arg	Gly	Glu	Tyr	Ile	Asp	Asn	Arg	Ser	Ser	Gln	Arg	His	115	120	125	
	Ser	Pro	Pro	Phe	Ser	Lys	Thr	Leu	Pro	Ser	Lys	Pro	Ser	Trp	Pro	Ser	130	135	140	
	Glu	Lys	Ala	Arg	Leu	Thr	Ser	Thr	Leu	Pro	Ala	Leu	Thr	Ala	Leu	Gln	145	150	155	160
35	Lys	Pro	Gln	Val	Pro	Pro	Lys	Pro	Lys	Gly	Leu	Leu	Glu	Asp	Glu	Ala	165	170	175	
	Asp	Tyr	Val	Val	Pro	Val	Glu	Asp	Asn	Asp	Glu	Asn	Tyr	Ile	His	Pro	180	185	190	
40	Thr	Glu	Ser	Ser	Ser	Pro	Pro	Pro	Glu	Lys	Ala	Pro	Met	Val	Asn	Arg	195	200	205	
	Ser	Thr	Lys	Pro	Asn	Ser	Ser	Thr	Pro	Ala	Ser	Pro	Pro	Gly	Thr	Ala	210	215	220	
	Ser	Gly	Arg	Asn	Ser	Gly	Ala	Trp	Glu	Thr	Lys	Ser	Pro	Pro	Pro	Ala	225	230	235	240
50	Ala	Pro	Ser	Pro	Leu	Pro	Arg	Ala	Gly	Lys	Lys	Pro	Thr	Thr	Pro	Leu	245	250	255	
	Lys	Thr	Thr	Pro	Val	Ala	Ser	Gln	Gln	Asn	Ala	Ser	Ser	Val	Cys	Glu	260	265	270	

55

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	Glu Lys Pro Ile Pro Ala Glu Arg His Arg Gly Ser Ser His Arg Gln	
	275	280 285
5	Glu Ala Val Gln Ser Pro Val Phe Pro Pro Ala Gln Lys Gln Ile His	
	290	295 300
	Gln Lys Pro Ile Pro Leu Pro Arg Phe Thr Glu Gly Gly Asn Pro Thr	
	305	310 315 320
10	Val Asp Gly Pro Leu Pro Ile Phe Ser Ser Asn Ser Thr Ile Ser Glu	
		325 330 335
	Gln Glu Ala Gly Val Leu Cys Lys Pro Trp Tyr Ala Gly Ala Cys Asp	
		340 345 350
15	Arg Lys Ser Ala Glu Glu Ala Leu His Arg Ser Asn Lys Asp Gly Ser	
		355 360 365
	Phe Leu Ile Arg Lys Ser Ser Gly His Asp Ser Lys Gln Pro Tyr Thr	
20		370 375 380
	Leu Val Val Phe Phe Asn Lys Arg Val Tyr Asn Ile Pro Val Arg Phe	
	385	390 395 400
25	Ile Glu Ala Thr Lys Gln Tyr Ala Leu Gly Arg Lys Lys Asn Gly Glu	
		405 410 415
	Glu Tyr Phe Gly Ser Val Ala Glu Ile Ile Arg Asn His Gln His Ser	
		420 425 430
30	Pro Leu Val Leu Ile Asp Ser Gln Asn Asn Thr Lys Asp Ser Thr Arg	
		435 440 445
	Leu Lys Tyr Ala Val Lys Val Ser	
35		450 455

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1806 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

50	CCTTCGTGGC CGCAGCCTGC ACTCTCAGAA ATCAGACTTG AGTGGCCGGA ACCCTTGAGA	60
	CCAGAGGCTT ACCATGCTGC TCCCTAGGAG GGCCAGGAAC TGCTGACGTG ACCACTGGAC	120
	AGTTATTCGT GTCTCTTACA ATTACCAAAC AGAATGGACA AGCTTAATAA AATAACCGTC	180
55	CCCGCCAGTC AGAAGTTGAG GCAGCTTCAA AAGATGGTCC ATGATATTAA AAACAATGAA	240

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GGTGGAATAA TGAATAAAAT CAAAAAGCTA AAAGTCAAAG CACCTCCAAG TGTTCCTCGA 300

AGGGACTACG CTTTCAGAGAG CCCCGCTGAC GAAGAGGAGC AGTGGTCCGA TGACTTTGAC 360

5 AGCGACTATG AAAATCCAGA TGAGCACTCG GACTCAGAGA TGTACGTGAT GCCCGCCGAG 420

GAGAACGCTG ATGACAGCTA CGAGCCGCCT CCAGTAGAGC AGGAAACCAG GCCGGTTCAC 480

10 CCAGCCCTGC CCTTCGCCAG AGGCGAGTAT ATAGACAATC GATCAAGCCA GAGGCATTCC 540

CCACCCTTCA GCAAGACACT TCCCAGTAAG CCCAGCTGGC CTTTCAGAGAA AGCAAGGCTC 600

ACCTCCACCC TGCCGGCCCT GACTGCTTTG CAGAAACCTC AAGTCCCACC CAAACCCAAA 660

15 GGCCTCCTTG AGGATGAGGC TGATTATGTG GTCCCCGTGG AAGATAATGA TGAAACTAT 720

ATTCATCCCA CAGAAAGCAG TTCACCTCCA CCTGAAAAAG CTCCCATGGT GAATAGATCA 780

20 ACCAAGCCAA ATTCCTCAAC GCCCGCCTCT CCTCCAGGAA CAGCTTCAGG TCGAAACAGT 840

GGGGCCTGGG AAACCAAGTC ACCTCCACCA GCTGCACCAT CCCCGTTGCC ACGGGCCGGG 900

AAAAAACCAA CGACACCACT GAAGACAACT CCAGTTGCCT CTCAACAGAA TGCTTCAAGT 960

25 GTTTGTGAAG AAAAACCTAT ACCTGCTGAA CGCCACCGAG GGTCAAGTCA CAGACAAGAA 1020

GCTGTGCAGT CACCAGTGTT TCCTCCTGCC CAGAAACAAA TCCACCAAAA ACCCATACCT 1080

30 CTGCCAAGAT TTACAGAAGG GGGAAACCCA ACTGTGGATG GGCCCCCTACC CAGCTTTTCA 1140

TCTAATTCCA CTATTTTCAGA ACAGGAAGCT GGCGTTCTCT GCAAGCCATG GTATGCTGGA 1200

GCCTGTGATC GAAAGTCTGC TGAAGAGGCA TTGCACAGAT CAAACAAGGA TGGATCATTT 1260

35 CTTATTCGGA AAAGCTCTGG CCATGATTCC AAACAACCAT ATACACTAGT TGTATTCTTT 1320

AATAAGCGAG TATATAATAT TCCTGTGCGA TTTATTGAAG CAACAAAACA ATATGCCTTG 1380

40 GGCAGAAAGA AAAATGGTGA AGAGTACTTT GGAAGTGTTG CTGAAATCAT CAGGAATCAT 1440

CAACATAGTC CTTTGGTTCT TATTGACAGT CAGAATAACA CAAAAGATTC CACCAGACTG 1500

AAGTATGCAG TTAAAGTTTC ATAAAGGGGG AAAAAAAGA TCAATACCAT TGCTTCAGAC 1560

45 ACTTTCCCAA AGTTTCTCCT TTTGAGAAAA AGTCCCAAAA CTTCATATTT TGGATTATGA 1620

ATCATCCAGT AATAAAATGG AAGATGGAGT CAGCTATTGA AGTGGTCATC CATTTCTTTT 1680

50 TAAGAAGCTC ATGTGGA CTTTCTATTGC CTGACCTGAT GAACTGTTAA TATCTGGTGA 1740

GGTTGAGTTA TCATGCTACT AATATTTTCC AAATAAATAT TTTTATTTTT AAAAAAAAAA 1800

AAAAAA 1806

55 (2) INFORMATION FOR SEQ ID NO:3:

-32-

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

5

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

10

Met Asp Lys Leu Asn Lys Ile Thr Val Pro Ala Ser Gln Lys Leu Arg
 1 5 10 15

15

His Ile Lys Asn Asn Glu Gly Gly Ile Met Asn Lys Ile Lys Lys Leu
 20 25 30

Lys Val Lys Ala Pro Pro Ser Val Pro Arg Arg Asp Tyr Ala Ser Glu
 35 40 45

20

Ser Pro Ala Asp Glu Glu Glu Gln Trp Ser Asp Asp Phe Asp Ser Asp
 50 55 60

25

Tyr Glu Asn Pro Asp Glu His Ser Asp Ser Glu Met Tyr Val Met Pro
 65 70 75 80

Ala Glu Glu Asn Ala Asp Asp Ser Tyr Glu Pro Pro Pro Val Glu Gln
 85 90 95

30

Glu Thr Arg Pro Val His Pro Ala Leu Pro Phe Ala Arg Gly Glu Tyr
 100 105 110

Ile Asp Asn Arg Ser Ser Gln Arg His Ser Pro Pro Phe Ser Lys Thr
 115 120 125

35

Leu Pro Ser Lys Pro Ser Trp Pro Ser Glu Lys Ala Arg Leu Thr Ser
 130 135 140

40

Thr Leu Pro Ala Leu Thr Ala Leu Gln Lys Pro Gln Val Pro Pro Lys
 145 150 155 160

Pro Lys Gly Leu Leu Glu Asp Glu Ala Asp Tyr Val Val Pro Val Glu
 165 170 175

45

Asp Asn Asp Glu Asn Tyr Ile His Pro Thr Glu Ser Ser Ser Pro Pro
 180 185 190

Pro Glu Lys Ala Pro Met Val Asn Arg Ser Thr Lys Pro Asn Ser Ser
 195 200 205

50

Thr Pro Ala Ser Pro Pro Gly Thr Ala Ser Gly Arg Asn Ser Gly Ala
 210 215 220

Trp Glu Thr Lys Ser Pro Pro Pro Ala Ala Pro Ser Pro Leu Pro Arg
 225 230 235 240

55

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Ala Gly Lys Lys Pro Thr Thr Pro Leu Lys Thr Thr Pro Val Ala Ser
245 250 255

5 Gln Gln Asn Ala Ser Ser Val Cys Glu Glu Lys Pro Ile Pro Ala Glu
260 265 270

Arg His Arg Gly Ser Ser His Arg Gln Glu Ala Val Gln Ser Pro Val
275 280 285

10 Phe Pro Pro Ala Gln Lys Gln Ile His Gln Lys Pro Ile Pro Leu Pro
290 295 300

Arg Phe Thr Glu Gly Gly Asn Pro Thr Val Asp Gly Pro Leu Pro Ser
305 310 315 320

15 Phe Ser Ser Asn Ser Thr Ile Ser Glu Gln Glu Ala Gly Val Leu Cys
325 330 335

Lys Pro Trp Tyr Ala Gly Ala Cys Asp Arg Lys Ser Ala Glu Glu Ala
340 345 350

20 Leu His Arg Ser Asn Lys Asp Gly Ser Phe Leu Ile Arg Lys Ser Ser
355 360 365

25 Gly His Asp Ser Lys Gln Pro Tyr Thr Leu Val Val Phe Phe Asn Lys
370 375 380

Arg Val Tyr Asn Ile Pro Val Arg Phe Ile Glu Ala Thr Lys Gln Tyr
385 390 395 400

30 Ala Leu Gly Arg Lys Lys Asn Gly Glu Glu Tyr Phe Gly Ser Val Ala
405 410 415

Glu Ile Ile Arg Asn His Gln His Ser Pro Leu Val Leu Ile Asp Ser
420 425 430

35 Gln Asn Asn Thr Lys Asp Ser Thr Arg Leu Lys Tyr Ala Val Lys Val
435 440 445

40 Ser

(2) INFORMATION FOR SEQ ID NO:4:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1785 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

- 50 (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

55 CCTTCGTGGC CGCAGCCTGC ACTCTCAGAA ATCAGACTTG AGTGGCCGGA ACCCTTGAGA

60

	CCAGAGGCTT	ACCATGCTGC	TCCCTAGGAG	GGCCAGGAAC	TGCTGACGTG	ACCACTGGAC	120
	AGTTATTCGT	GTCTCTTACA	ATTACCAAAC	AGAATGGACA	AGCTTAATAA	AATAACCGTC	180
5	CCCGCCAGTC	AGAAGTTGAG	GCATATTAAA	AACAATGAAG	GTGGAATAAT	GAATAAAATC	240
	AAAAAGCTAA	AAGTCAAAGC	ACCTCCAAGT	GTTCTCTGAA	GGGACTACGC	TTCAGAGAGC	300
	CCCGCTGACG	AAGAGGAGCA	GTGGTCCGAT	GACTTTGACA	GCGACTATGA	AAATCCAGAT	360
10	GAGCACTCGG	ACTCAGAGAT	GTACGTGATG	CCCGCCGAGG	AGAACGCTGA	TGACAGCTAC	420
	GAGCCGCCTC	CAGTAGAGCA	GGAAACCAGG	CCGGTTCACC	CAGCCCTGCC	CTTCGCCAGA	480
15	GGCGAGTATA	TAGACAATCG	ATCAAGCCAG	AGGCATTCCC	CACCCTTCAG	CAAGACACTT	540
	CCCAGTAAGC	CCAGCTGGCC	TTCAGAGAAA	GCAAGGCTCA	CCTCCACCCT	GCCGGCCCTG	600
	ACTGCTTTGC	AGAAACCTCA	AGTCCCACCC	AAACCCAAAG	GCCTCCTTGA	GGATGAGGCT	660
20	GATTATGTGG	TCCCCGTGGA	AGATAATGAT	GAAAACTATA	TTCATCCCAC	AGAAAGCAGT	720
	TCACCTCCAC	CTGAAAAAGC	TCCCATGGTG	AATAGATCAA	CCAAGCCAAA	TTCCTCAACG	780
25	CCCGCCTCTC	CTCCAGGAAC	AGCTTCAGGT	CGAAACAGTG	GGGCCTGGGA	AACCAAGTCA	840
	CCTCCACCAG	CTGCACCATC	CCCGTTGCCA	CGGGCCGGGA	AAAAACCAAC	GACACCACTG	900
	AAGACAATC	CAGTTGCCTC	TCAACAGAAT	GCTTCAAGTG	TTTGTGAAGA	AAAACCTATA	960
30	CCTGCTGAAC	GCCACCGAGG	GTCAAGTCAC	AGACAAGAAG	CTGTGCAGTC	ACCAGTGTTT	1020
	CCTCCTGCCC	AGAAACAAAT	CCACCAAAAA	CCCATACCTC	TGCCAAGATT	TACAGAAGGG	1080
35	GGAAACCCAA	CTGTGGATGG	GCCCCTACCC	AGCTTTTCAT	CTAATTCCAC	TATTTAGAA	1140
	CAGGAAGCTG	GCGTTCTCTG	CAAGCCATGG	TATGCTGGAG	CCTGTGATCG	AAAGTCTGCT	1200
	GAAGAGGCAT	TGCACAGATC	AAACAAGGAT	GGATCATTTT	TTATTCGGAA	AAGCTCTGGC	1260
40	CATGATTCCA	AACAACCATA	TACACTAGTT	GTATTCTTTA	ATAAGCGAGT	ATATAATATT	1320
	CCTGTGCGAT	TTATTGAAGC	AACAAAACAA	TATGCCTTGG	GCAGAAAGAA	AAATGGTGAA	1380
45	GAGTACTTTG	GAAGTGTTGC	TGAAATCATC	AGGAATCATC	AACATAGTCC	TTGGTTCTT	1440
	ATTGACAGTC	AGAATAACAC	AAAAGATTCC	ACCAGACTGA	AGTATGCAGT	TAAAGTTTCA	1500
	TAAAGGGGGA	AAAAAAAGAT	CAATACCATT	GCTTCAGACA	CTTTCCCAA	GTTTCTCCTT	1560
50	TTGAGAAAAA	GTCCCAAAC	TTCATATTTT	GGATTATGAA	TCATCCAGTA	ATAAAATGGA	1620
	AGATGGAGTC	AGCTATTGAA	GTGGTCATCC	ATTTCTTTTT	AAGAAGCTCA	TGTGGACTTG	1680
55	TTCTATTGCC	TGACCTGATG	AACTGTTAAT	ATCTGGTGAG	GTTGAGTTAT	CATGCTACTA	1740

ATATTTTCCA AATAAATATT TTTATTTTAA AAAAAAAAAA AAAAA

1785

(2) INFORMATION FOR SEQ ID NO:5:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 457 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

15	Met	Asp	Lys	Leu	Asn	Lys	Ile	Thr	Val	Pro	Ala	Ser	Gln	Lys	Leu	Arg	1	5	10	15
	Gln	Leu	Gln	Lys	Met	Val	His	Asp	Ile	Lys	Asn	Asn	Glu	Gly	Gly	Ile	20	25	30	
20	Met	Asp	Lys	Ile	Lys	Lys	Leu	Lys	Val	Lys	Gly	Pro	Pro	Ser	Val	Pro	35	40	45	
	Arg	Arg	Asp	Tyr	Ala	Leu	Asp	Ser	Pro	Ala	Asp	Glu	Glu	Glu	Gln	Trp	50	55	60	
	Ser	Asp	Asp	Phe	Asp	Ser	Asp	Tyr	Glu	Asn	Pro	Asp	Glu	His	Ser	Asp	65	70	75	80
30	Ser	Glu	Met	Tyr	Val	Met	Pro	Ala	Glu	Glu	Thr	Gly	Asp	Asp	Ser	Tyr	85	90	95	
	Glu	Pro	Pro	Pro	Ala	Glu	Gln	Gln	Thr	Arg	Val	Val	His	Pro	Ala	Leu	100	105	110	
35	Pro	Phe	Thr	Arg	Gly	Glu	Tyr	Val	Asp	Asn	Arg	Ser	Ser	Gln	Arg	His	115	120	125	
	Ser	Pro	Pro	Phe	Ser	Lys	Thr	Leu	Pro	Ser	Lys	Pro	Ser	Trp	Pro	Ser	130	135	140	
	Ala	Lys	Ala	Arg	Leu	Ala	Ser	Thr	Leu	Pro	Ala	Pro	Asn	Ser	Leu	Gln	145	150	155	160
45	Lys	Pro	Gln	Val	Pro	Pro	Lys	Pro	Lys	Asp	Leu	Leu	Glu	Asp	Glu	Ala	165	170	175	
	Asp	Tyr	Val	Val	Pro	Val	Glu	Asp	Asn	Asp	Glu	Asn	Tyr	Ile	His	Pro	180	185	190	
50	Arg	Glu	Ser	Ser	Pro	Pro	Pro	Ala	Glu	Lys	Ala	Pro	Met	Val	Asn	Arg	195	200	205	
	Ser	Thr	Lys	Pro	Asn	Ser	Ser	Ser	Lys	His	Met	Ser	Pro	Pro	Gly	Thr	210	215	220	

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	Val	Ala	Gly	Arg	Asn	Ser	Gly	Val	Trp	Asp	Ser	Lys	Ser	Ser	Leu	Pro
	225					230					235					240
5	Ala	Ala	Pro	Ser	Pro	Leu	Pro	Arg	Ala	Gly	Lys	Lys	Pro	Ala	Thr	Pro
					245					250					255	
	Leu	Lys	Thr	Thr	Pro	Val	Pro	Pro	Leu	Pro	Asn	Ala	Ser	Asn	Val	Cys
				260					265					270		
10	Glu	Glu	Lys	Pro	Val	Pro	Ala	Glu	Arg	His	Arg	Gly	Ser	Ser	His	Arg
			275					280					285			
	Gln	Asp	Thr	Val	Gln	Ser	Pro	Val	Phe	Pro	Pro	Thr	Gln	Lys	Pro	Val
		290					295					300				
15	His	Gln	Lys	Pro	Val	Pro	Leu	Pro	Arg	Phe	Pro	Glu	Ala	Gly	Ser	Pro
	305					310				315						320
	Ala	Ala	Asp	Gly	Pro	Phe	His	Ser	Phe	Pro	Phe	Asn	Leu	Thr	Phe	Ala
20					325					330					335	
	Asp	Gln	Glu	Gly	Glu	Leu	Leu	Gly	Lys	Pro	Trp	Tyr	Ala	Gly	Ala	Cys
				340					345					350		
25	Asp	Arg	Lys	Phe	Ala	Glu	Glu	Ala	Leu	His	Arg	Ser	Asn	Lys	Asp	Gly
			355					360					365			
	Ser	Phe	Leu	Ile	Arg	Lys	Ser	Phe	Gly	His	Asp	Ser	Lys	Gln	Pro	Tyr
		370					375					380				
30	Thr	Leu	Val	Ala	Phe	Phe	Asn	Lys	Arg	Val	Tyr	Asn	Ile	Pro	Val	Arg
	385					390					395					400
	Phe	Ile	Glu	Ala	Thr	Lys	Gln	Tyr	Ala	Leu	Gly	Lys	Lys	Lys	Asn	Gly
35					405					410					415	
	Glu	Glu	Tyr	Phe	Gly	Ser	Val	Val	Glu	Ile	Val	Asn	Ser	His	Gln	His
				420					425					430		
40	Asn	Pro	Leu	Val	Leu	Ile	Asp	Ser	Gln	Asn	Asn	Thr	Lys	Asp	Ser	Thr
			435					440					445			
	Arg	Leu	Lys	Tyr	Ala	Val	Lys	Val	Ser							
45				450				455								

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1718 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

	CTGTGGGTTG	CTCGCAGAAG	TCAGTTCCAG	TGGCTTGAGT	TCTTGAGGCC	AGAGCCTTAC	60
	CATGCTGCTC	CCCAGGAAGT	CCAGGAGCTG	CTGACACCCC	CCTGGACAGC	GACACATCCT	120
5	CTCTCAAGAA	AATGGACAAG	CTGAATAAGA	TAACTGTCCC	TGCCAGCCAG	AAGCTGAGAC	180
	AGCTTCAAAA	GATGGTCCAT	GATATTAAGA	ACAATGAAGG	TGGAATAATG	GACAAGATAA	240
	AAAAGCTAAA	AGTCAAAGGC	CCTCCAAGTG	TTCCTCGAAG	GGACTATGCA	TTAGACAGCC	300
10	CTGCAGATGA	AGAGGAGCAG	TGGTCAGATG	ACTTCGACAG	TGACTATGAA	AATCCAGATG	360
	AACATTCGGA	CTCCGAGATG	TATGTGATGC	CTGCCGAGGA	GACGGGCGAC	GATTCCTATG	420
15	AACCGCCTCC	CGCTGAGCAG	CAGACACGGG	TGGTCCATCC	AGCCCTGCCC	TTCACGAGGG	480
	GCGAGTATGT	AGATAATCGA	TCCAGCCAGC	GGCACTCTCC	GCCCTTCAGC	AAGACACTTC	540
	CCAGTAAGCC	CAGCTGGCCT	TCAGCGAAAG	CGAGGCTGGC	CTCCACTCTG	CCAGCCCCCA	600
20	ACTCTCTACA	GAAGCCTCAA	GTCCCCCCCCA	AGCCCAAAGA	CCTCCTTGAG	GATGAGGCTG	660
	ATTATGTGGT	CCCTGTGGAA	GATAACGATG	AAAACATAT	CCATCCCAGA	GAAAGTAGCC	720
25	CGCCGCCTGC	TGAGAAGGCT	CCCATGGTGA	ATAGATCAAC	CAAGCCAAAC	AGTTCCTCAA	780
	AGCACATGTC	GCCTCCAGGG	ACTGTCGCAG	GTCGAAACAG	TGGGGTCTGG	GACTCCAAGT	840
	CATCTTTGCC	TGCCGCACCA	TCCCCACTAC	CACGGGCTGG	GAAGAAGCCA	GCTACACCAC	900
30	TTAAGACTAC	TCCCGTTCCT	CCCCTACCGA	ATGCATCAAA	TGTTTGTGAA	GAAAAGCCTG	960
	TTCCTGCTGA	GCGCCACCGA	GGGTCTAGTC	ACAGACAAGA	CACTGTACAG	TCACCAGTGT	1020
35	TTCCTCCCAC	CCAGAAACCT	GTCCATCAAA	AGCCTGTACC	CTTGCCAAGG	TTCCCAGAAG	1080
	CGGGGAGCCC	AGCTGCAGAT	GGACCGTTCC	ACAGCTTCCC	ATTTAATTTG	ACGTTTGCAG	1140
	ACCAGGAGGG	TGAACTGCTC	GGTAAGCCCT	GGTATGCTGG	CGCCTGTGAC	CGCAAGTTTG	1200
40	CTGAAGAGGC	CTTGACACAGA	TCCAACAAGG	ATGGATCGTT	TCTTATTCGG	AAGAGCTTTG	1260
	GCCATGATTC	CAAGCAGCCG	TACACCCTAG	TTGCGTTCTT	TAACAAGCGA	GTGTATAATA	1320
45	TTCCTGTACG	GTTTATTGAA	GCAACCAAAC	AGTATGCTTT	GGGAAAGAAG	AAAAATGGTG	1380
	AAGAGTACTT	CGGAAGTGTT	GTGGAAATCG	TCAACAGTCA	TCAGCACAAAC	CCCCTGGTTC	1440
	TTATTGACAG	TCAGAATAAC	ACGAAAGATT	CCACGAGACT	GAAATATGCT	GTGAAGGTTT	1500
50	CATAACGATA	CCACGGTTCC	AGACATGTCC	TCTGTTTCTT	CTTTTGAGAA	AACATCATAT	1560
	TCTGGCTATG	ACTCCTCAGC	AGTAAGAGAG	AAAAGATGAA	TGAAGCCACT	GAGGCTTCGT	1620
55	GAATGAATGA	ATCTACTCCT	TCCTAGGGCG	TTCACACGAG	CTTTTCTATC	ACCTGACCTG	1680

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ACGAAGTCAT AGCTGGGGAG GTTCGGTTAC TATGATAC

1718

(2) INFORMATION FOR SEQ ID NO:7:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

15 Tyr Glu Xaa Pro
 1

(2) INFORMATION FOR SEQ ID NO:8:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 30 (B) LOCATION: 1..2
 (D) OTHER INFORMATION: /note= "The 'X' appearing at
 positions 1, 8 and 15, represent either Aspartic Acid or
 Glutamic Acid."

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Xaa Xaa Tyr Glu Xaa Pro Xaa Xaa Xaa Tyr Xaa Xaa Pro Xaa Xaa Xaa
 1 5 10 15

40 Tyr Glu Pro Pro
 20

(2) INFORMATION FOR SEQ ID NO:9:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

50

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 55 (B) LOCATION: 19..20

-39-

(D) OTHER INFORMATION: /note= "The 'N' at position 19 represents Inosine."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

5

TCGAGAATTC AARAARCCNA CNACNCC

27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

20 Lys Lys Pro Thr Thr Pro Leu Lys
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: misc_feature

35 (B) LOCATION: 13..14

(D) OTHER INFORMATION: /note= "The 'N' at position 13 represents Inosine."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

40

CTGAGGATCC TTNGTNGCYT CDATRAA

27

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

50

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

55 Lys Arg Val Tyr Asn Ile Pro Val Arg Phe Ile Glu Ala Thr Lys
1 5 10 15

CLAIMS

We claim:

1. A recombinant nucleic acid encoding a BLNK protein.
2. A recombinant nucleic acid according to claim 1 that is at least 60% identical to the sequence depicted in Figure 2.
3. A recombinant nucleic acid according to claim 1 wherein said BLNK protein is a human BLNK protein.
4. A recombinant nucleic acid according to claim 1 encoding the amino acid sequence depicted in Figure 1.
5. A recombinant nucleic acid according to claim 1 which will hybridize to the nucleic acid depicted in Figure 2 under high stringency conditions.
6. A recombinant nucleic acid according to claim 1 comprising the nucleic acid depicted in Figure 2.
7. An expression vector comprising transcriptional and translational regulatory DNA operably linked to DNA encoding a BLNK protein.
8. A host cell transformed with the nucleic acid of claim 1.
9. A host cell transformed with an expression vector according to claim 7.
10. A method of producing a BLNK protein comprising:
 - a) culturing a host cell transformed with nucleic acid encoding a BLNK protein; and
 - b) expressing said nucleic acid to produce a BLNK protein.

11. A recombinant BLNK protein.
12. A recombinant BLNK protein according to claim 11 encoded by a nucleic acid which hybridizes to the nucleic acid sequence shown in Figure 2 under high stringency conditions.
13. A recombinant BLNK protein according to claim 11 encoded by a nucleic acid which is at least 60% identical to the nucleic acid sequence shown in Figure 2.
14. A recombinant BLNK protein according to claim 11 which is at least about 50% homologous to the amino acid sequence shown in Figure 1.
15. A recombinant BLNK protein according to claim 11 which has the amino acid sequence shown in Figure 1.
16. A pharmaceutical composition comprising a BLNK protein.
17. A polypeptide capable of specifically binding to a BLNK 1 protein.
18. A polypeptide according to claim 17 wherein said polypeptide is an antibody.
19. An antibody which binds a BLNK protein.
20. A method for detecting a BLNK protein in a target sample comprising contacting a labelled polypeptide according to claim 17 with said target sample and assaying for the presence of binding between said labelled polypeptide and BLNK, if present, in said target sample.
21. A method for screening for a bioactive agent capable of binding to a BLNK protein, said method comprising combining a BLNK protein and a candidate bioactive agent, and determining the binding of said candidate agent to BLNK protein.

22. A method for screening for a bioactive agent capable of modulating the bioactivity of a BLNK protein, said method comprising the steps of:

a) combining:

i) a BLNK protein;

ii) a candidate bioactive agent; and

iii) a protein selected from the group consisting of Grb2 and PLC- γ ; and

b) determining the binding of said protein to said BLNK protein;

wherein the absence of binding of said protein to said BLNK protein indicates that said agent is capable of modulating the bioactivity of said BLNK protein.

1/9

Predicted amino acid sequence of human BLNK-1: 1-456

MDKLNKITTVPASQKLRLQKQMVHDIKNNEGIMNKIKLKVKAPPSVPRRDYASESPADEEEQ
WSDDFDSDYENPDEHSDSEMYVMPAEENADDSEYPPVEQETRPVHPALPFARGEYIDNRSSQ
RHSPFFSKTLPSPKPSWPSEKARLTSTLPALTALQKPQVPPKPKGLLEDEADYVVPVEDNDENY
IHPTSSSSPPPEKAPMVNRSSTKPNSSSTPASPPGTASGRNSGAWETKSPPPAAPSPPLPRAGKKP
TTPLKTTTPVASQQNASSVCEEKPIPAERHRGSSHRQEAQSPVFPQAQKQIHQKPIPLPRFTE
GGNPTVDGPLPIFSSNSTISEQEAGVLCCKPWYAGACDRKSAEEALHRSNKDGSFLIRKSSGHD
SKQPYTTLVFFNKRVTNIPVRFIEATKQYALGRKKNGEYFGSVAEIIRNHQHSPLVLIDSQN
NTKDSTRLLKYAVKVS*

Fig. 1

cDNA Sequence of human.BLNK-1:

Open Reading Frame: 154 - 1524

CCTTCGTGGCCGCAGCCTGCACTCTCAGAAATCAGACTTGAGTGGCCGGAACCCTTGAGACCA
GAGGCTTACCATGCTGCTCCCTAGGAGGGCCAGGAAGTCTGACGTGACCACTGGACAGTTAT
TCGTGTCTCTTACAATTACCAAACAGAATGGACAAGCTTAATAAAATAACCGTCCCCGCCAGT
CAGAAGTTGAGGCAGCTTCAAAAGATGGTCCATGATATTAAAAACAATGAAGGTGGAATAATG
AATAAAATCAAAAAGCTAAAAGTCAAAGCACCTCCAAGTGTTCCTCGAAGGGACTACGCTTCA
GAGAGCCCCGCTGACGAAGAGGAGCAGTGGTCCGATGACTTTGACAGCGACTATGAAAATCCA
GATGAGCACTCGGACTCAGAGATGTACGTGATGCCCGCCGAGGAGAACGCTGATGACAGCTAC
GAGCCGCCTCCAGTAGAGCAGGAAACCAGGCGCGTTACCCAGCCCTGCCCTTCGCCAGAGGC
GAGTATATAGACAATCGATCAAGCCAGAGGCATTCCCCACCCTTCAGCAAGACACTTCCCAGT
AAGCCCAGCTGGCCTTCAGAGAAAGCAAGGCTCACCTCCACCCTGCCGGCCCTGACTGCTTTG
CAGAAACCTCAAGTCCCACCCAAACCCAAAGGCCTCCTTGAGGATGAGGCTGATTATGTGGTC
CCCGTGGAAGATAATGATGAAAACCTATATTCATCCACAGAAAGCAGTTACCTCCACCTGAA
AAAGCTCCCATGGTGAATAGATCAACCAAGCCAAATTCCTCAACGCCCGCCTCTCCTCCAGGA
ACAGCTTCAGGTGCAACAGTGGGGCCTGGGAAACCAAGTCACCTCCACCAGCTGCACCATCC
CCGTTGCCACGGGCCGGGAAAAACCAACGACACCACTGAAGACAACCTCCAGTTGCCTCTCAA
CAGAATGCTTCAAGTGTTTGTGAAGAAAAACCTATACCTGCTGAACGCCACCGAGGGTCAAGT
CACAGACAAGAAGCTGTGCAGTCACCAGTGTTTCCTCCTGCCCAGAAACAAATCCACCAAAAA
CCCATACCTCTGCCAAGATTTACAGAAGGGGGAAACCCAACTGTGGATGGGCCCCCTACCCAGC
TTTTCATCTAATTCCACTATTTACAGAACAGGAAGCTGGCGTTCTCTGCAAGCCATGGTATGCT
GGAGCCTGTGATCGAAAGTCTGCTGAAGAGGCATTGCACAGATCAAACAAGGATGGATCATTT
CTTATTCGGAAAAGCTCTGGCCATGATTCCAAACAACCATATACACTAGTTGTATTCTTTAAT
AAGCGAGTATATAATATTCCTGTGCGATTTATTGAAGCAACAAAACAATATGCCTTGGGCAGA
AAGAAAAATGGTGAAGAGTACTTTGGAAGTGTTGCTGAAATCATCAGGAATCATCAACATAGT
CCTTTGGTTCTTATTGACAGTCAGAATAACACAAAAGATTCCACCAGACTGAAGTATGCAGTT
AAAGTTTCATAAAGGGGGGAAAAAAAAGATCAATACCATTGCTTCAGACACTTTCCCAAAGTTT
CTCCTTTTGAGAAAAAGTCCCAAAACTTCATATTTTGGATTATGAATCATCCAGTAATAAAAT
GGAAGATGGAGTCAGCTATTGAAGTGGTCATCCATTTCTTTTAAAGAAGCTCATGTGGACTTG
TTCTATTGCCTGACCTGATGAACTGTTAATATCTGGTGAGGTTGAGTTATCATGCTACTAATA
TTTTCCAAATAAATATTTTATTTTAAAAAATAAAAAAAAAA

Fig. 2

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OPEN READING FRAME OF HUMAN BLNK 2

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Met Asp Lys Leu Asn Lys Ile Thr Val Pro Ala Ser Gln Lys Leu Arg
1           5           10           15

His Ile Lys Asn Asn Glu Gly Gly Ile Met Asn Lys Ile Lys Lys Leu
20           25           30

Lys Val Lys Ala Pro Pro Ser Val Pro Arg Arg Asp Tyr Ala Ser Glu
35           40           45

Ser Pro Ala Asp Glu Glu Glu Gln Trp Ser Asp Asp Phe Asp Ser Asp
50           55           60

Tyr Glu Asn Pro Asp Glu His Ser Asp Ser Glu Met Tyr Val Met Pro
65           70           75           80

Ala Glu Glu Asn Ala Asp Asp Ser Tyr Glu Pro Pro Pro Val Glu Gln
85           90           95

Glu Thr Arg Pro Val His Pro Ala Leu Pro Phe Ala Arg Gly Glu Tyr
100          105          110

Ile Asp Asn Arg Ser Ser Gln Arg His Ser Pro Pro Phe Ser Lys Thr
115          120          125

Leu Pro Ser Lys Pro Ser Trp Pro Ser Glu Lys Ala Arg Leu Thr Ser
130          135          140

Thr Leu Pro Ala Leu Thr Ala Leu Gln Lys Pro Gln Val Pro Pro Lys
145          150          155          160

Pro Lys Gly Leu Leu Glu Asp Glu Ala Asp Tyr Val Val Pro Val Glu
165          170          175

Asp Asn Asp Glu Asn Tyr Ile His Pro Thr Glu Ser Ser Ser Pro Pro
180          185          190

Pro Glu Lys Ala Pro Met Val Asn Arg Ser Thr Lys Pro Asn Ser Ser
195          200          205

Thr Pro Ala Ser Pro Pro Gly Thr Ala Ser Gly Arg Asn Ser Gly Ala
210          215          220

Trp Glu Thr Lys Ser Pro Pro Pro Ala Ala Pro Ser Pro Leu Pro Arg
225          230          235          240

```

Ala Gly Lys Lys Pro Thr Thr Pro Leu Lys Thr Thr Pro Val Ala Ser
245 250 255

Gln Gln Asn Ala Ser Ser Val Cys Glu Glu Lys Pro Ile Pro Ala Glu
260 265 270

Arg His Arg Gly Ser Ser His Arg Gln Glu Ala Val Gln Ser Pro Val
275 280 285

Phe Pro Pro Ala Gln Lys Gln Ile His Gln Lys Pro Ile Pro Leu Pro
290 295 300

Arg Phe Thr Glu Gly Gly Asn Pro Thr Val Asp Gly Pro Leu Pro Ser
305 310 315 320

Phe Ser Ser Asn Ser Thr Ile Ser Glu Gln Glu Ala Gly Val Leu Cys
325 330 335

Lys Pro Trp Tyr Ala Gly Ala Cys Asp Arg Lys Ser Ala Glu Glu Ala
340 345 350

Leu His Arg Ser Asn Lys Asp Gly Ser Phe Leu Ile Arg Lys Ser Ser
355 360 365

Gly His Asp Ser Lys Gln Pro Tyr Thr Leu Val Val Phe Phe Asn Lys
370 375 380

Arg Val Tyr Asn Ile Pro Val Arg Phe Ile Glu Ala Thr Lys Gln Tyr
385 390 395 400

Ala Leu Gly Arg Lys Lys Asn Gly Glu Glu Tyr Phe Gly Ser Val Ala
405 410 415

Glu Ile Ile Arg Asn His Gln His Ser Pro Leu Val Leu Ile Asp Ser
420 425 430

Gln Asn Asn Thr Lys Asp Ser Thr Arg Leu Lys Tyr Ala Val Lys Val
435 440 445

Ser

Fig. 3B

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cDNA OF HUMAN BLNK 2

CCTTCGTGGC CGCAGCCTGC ACTCTCAGAA ATCAGACTTG AGTGGCCGGA ACCCTTGAGA 60
CCAGAGGCTT ACCATGCTGC TCCCTAGGAG GGCCAGGAAC TGCTGACGTG ACCACTGGAC 120
AGTTATTTCGT GTCTCTTACA ATTACCAAAC AGAATGGACA AGCTTAATAA AATAACCGTC 180
CCCGCCAGTC AGAAGTTGAG GCATATTAAA AACAAATGAAG GTGGAATAAT GAATAAAATC 240
AAAAAGCTAA AAGTCAAAGC ACCTCCAAGT GTTCCTCGAA GGGACTACGC TTCAGAGAGC 300
CCCGCTGACG AAGAGGAGCA GTGGTCCGAT GACTTTGACA GCGACTATGA AAATCCAGAT 360
GAGCACTCGG ACTCAGAGAT GTACGTGATG CCCGCCGAGG AGAACGCTGA TGACAGCTAC 420
GAGCCGCCTC CAGTAGAGCA GGAAACCAGG CCGGTTCAAC CAGCCCTGCC CTTCGCCAGA 480
GGCGAGTATA TAGACAATCG ATCAAGCCAG AGGCATTCCC CACCCTTCAG CAAGACACTT 540
CCCAGTAAGC CCAGCTGGCC TTCAGAGAAA GCAAGGCTCA CCTCCACCCT GCCGGCCCTG 600
ACTGCTTTGC AGAAACCTCA AGTCCCACCC AAACCCAAAG GCCTCCTTGA GGATGAGGCT 660
GATTATGTGG TCCCCGTGGA AGATAATGAT GAAAACTATA TTCATCCCAC AGAAAGCAGT 720
TCACCTCCAC CTGAAAAAGC TCCCATGGTG AATAGATCAA CCAAGCCAAA TTCCTCAACG 780
CCCGCCTCTC CTCCAGGAAC AGCTTCAGGT CGAAACAGTG GGGCCTGGGA AACCAAGTCA 840
CCTCCACCAG CTGCACCATC CCCGTTGCCA CGGGCCGGGA AAAAACCAAC GACACCACTG 900
AAGACAACCTC CAGTTGCCTC TCAACAGAAT GCTTCAAGTG TTTGTGAAGA AAAACCTATA 960
CCTGCTGAAC GCCACCGAGG GTCAAGTCAC AGACAAGAAG CTGTGCAGTC ACCAGTGTTT 1020
CCTCCTGCCC AGAAACAAAT CCACCAAAAA CCCATACCTC TGCCAAGATT TACAGAAGGG 1080
GGAAACCCAA CTGTGGATGG GCCCCTACCC AGCTTTTCAT CTAATTCCAC TATTTTCAGAA 1140
CAGGAAGCTG GCGTTCTCTG CAAGCCATGG TATGCTGGAG CCTGTGATCG AAAGTCTGCT 1200
GAAGAGGCAT TGCACAGATC AAACAAGGAT GGATCATTTT TTATTCGGAA AAGCTCTGGC 1260
CATGATTCCA AACAACCATA TACACTAGTT GTATTCTTTA ATAAGCGAGT ATATAATATT 1320
CCTGTGCGAT TTATTGAAGC AACAAAACAA TATGCCTTGG GCAGAAAGAA AAATGGTGAA 1380
GAGTACTTTG GAAGTGTTGC TGAAATCATC AGGAATCATC AACATAGTCC TTTGGTTCTT 1440
ATTGACAGTC AGAATAACAC AAAAGATTCC ACCAGACTGA AGTATGCAGT TAAAGTTTCA 1500
TAAAGGGGGA AAAAAAAGAT CAATACCATT GCTTCAGACA CTTTCCCAA GTTTCTCCTT 1560

Fig. 4A

TTGAGAAAAA	GTCCCAAAAC	TTCATATTTT	GGATTATGAA	TCATCCAGTA	ATAAAATGGA	1620
AGATGGAGTC	AGCTATTGAA	GTGGTCATCC	ATTTCTTTTT	AAGAAGCTCA	TGTGGACTTG	1680
TTCTATTGCC	TGACCTGATG	AACTGTTAAT	ATCTGGTGAG	GTTGAGTTAT	CATGCTACTA	1740
ATATTTTCCA	AATAAATATT	TTTATTTTTTA	AAAAAAAAAA	AAAAA		1785

Open reading frame of mouse BLNK.
MDKLNKITVPA SQKLRLQKQMVHDIKNNEGGIMDKIKLVKGPPSVPRRDYALDSPAD
EEEQWSDDFDSDYENPDEHSDSEMYVMPAEETGDDSYEPPEAEQQTRVWHPALPFTRGEY
VDNRSSQRHSPFSTLPSKPSWPSAKARLASTLPAPNSLQKPQVPPKPKDLEDEADYV
VPVEDNDENYIHPRESSPPAEKAPMVNRSTKPNSSSKHMSPPGTVAGRNSGVWDSKS
SLPAAPSPPLPRAGKKPATPLKTTTPVPLPNASNVCEEKVP/AERHSGSSHRQDTVQSPVF
PPTQKPVHQKPVPLPRFPEAGSPAADGPFHSPFNLTADQEGELLGKPWYAGACDRKFA
EEALHRSNKDGSFLIRKSFHSDSKQPYTLVAFFNKR VYNIPVRFIEATKQYALGKKKNGE
EYFGSVVEIVNSHQHNPLVLIDSQNNNTKDSIRLKYAVKVS

Fig. 5

cDNA of mouse BLNK.

CTGTGGTTGCTCGCAGAAGTCAGTCCAGTGGCTTGAGTTCTTGAGCCAGAGCCTT
 ACCATGCTGCTCCCAGGAAGTCCAGGAGCTGCTGACACCCCTGGACAGCGACAC
 ATCCTCTCAAGAAATGGACAAGCTGAATAAGATAACTGTCCCTGCCAGCCAGA
 AGCTGAGACAGCTTCAAAGATGGTCCATGATATTAAGAACAAATGAAGTGGAAT
 AATGGACAAGATAAAAGCTAAAGTCAAAGGCCCTCCAAGTGTCTCTCGAAGG
 GACTATGCATTAGACAGCCCTGCAGATGAAGAGGAGCAGTGCTCAGATGACTTCGA
 CAGTGACTATGAAAATCCAGATGAACATTCGGACTCCGAGATGTAATGTATGCTGC
 CGAGGAGACGGCGACGATTCTTACGAGGGCGAGTATGTAGATAATCGATCCAGCCA
 GGTCCATCCAGCCCTGCCCTTACGAGGGCGAGTATGTAGATAATCGATCCAGCCA
 GCGGCACTCTCCGCCCTTACGACAAGACACTTCCCAAGTAAAGCCAGCTGGCCTTACGCG
 AAAGCGAGGCTGGCCTCCACTTGCCAGCCCCCAACTCTCTACAGAAGCCTCAAGTCC
 CCCCCAAGCCCAAAGACCTCCTTGAGGATGAGGCTGATTATGTGGTCCCTGTGGAAG
 ATAACGATGAATACTATATCCATCCAGAGAAAGTACCCCGCCGCTGCTGAGAAG
 GCTCCCATGGTGAATAGATCAACCAAGCCAAACAGTTCCTCAAAGCACATGTGCGCCT
 CCAGGACTGTGCGAGTCCGAAACAGTGGGCTCTGGGACTCCAAAGTCACTTTGSCCT
 GCCGACCATCCCCACTACACGGGCTGGGAAGAACAGCTACACCACCTTAAGACT
 ACTCCCGTTCCCTACCGAATGCATCAAAATGTTGTGAAGAAAGCCTGTTCCTG
 CTGAGCGCCACCGAGGCTAGTCAAGACAGACACTGTACAGTACCAGTGTTC
 CTCCACCCAGAAACCTGTCCATCAAAGCCTGTACCTTGCCAAAGTTCCAGAAAG
 CGGGAGCCAGCTGCAGATGGACCGTTCCACAGCTTCCCATTTAATTGACGTTTGC
 AGACCAGGAGGTGAACCTGCTCGGTAAAGCCCTGGTATGCTGGCGCTGTGACCGCAA
 GTTGTGCTGAAGAGGCCCTTGACAGATCCAAAGGATGGATCGTTTCTTATTCGGAA
 GAGCTTTGGCCATGATTCCAAAGCAGCCGTACACCCCTAGTTGCGTTCTTAAACAAGCG
 AGTGTATAATATTCCTGTACGGTTTATTGAAGCAACCAACAGTATGCTTTGGGAA
 AGAAGAAAATGGTGAAGAGTACTTCGGAAAGTGTGTGGAAATCGTCAACAGTCA
 TCAGCACAAACCCCTGGTTCTTATTGACAGTCAGAAATAACACGAAAGATTCCACGAG
 ACTGAAATATGCTGTGAAGGTTTCATAACGATACCAAGTTCAGACATGTCTCTCTG
 TTTCTTCTTTTGAGAAAACATCATATTCTGGCTATGACTCCTCAGCAGTAAGAGAGA
 AAAGATGAATGAAGCCACTGAGGCTTCGTGAATGAATGAACTACTCCTCCTAGG
 GCGTTCACACGAGCTTTTCTATCACCTGACCTGACGAAGTCAATAGCTGGGAGGTTCC
 GTTACTATGATAC

Schematic of BLNK and BLNK-s.

BLNK



BLNK-s



Fig. 7

DECLARATION AND POWER OF ATTORNEY
FOR PATENT APPLICATION

As a below-named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled
BLNK PROTEINS

the specification of which

(check ☐ is attached hereto.
one)

☒ was filed as
PCT Application Serial No. PCT/US98/01394
on International Filing Date 23 January 1998.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose to the Patent Office all information known to me to be material to patentability as defined in 37 C.F.R. 1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

Prior Foreign Application(s)			Priority Claimed	
(Number)	(Country)	(Day/Month/Year Filed)	<input type="checkbox"/> Yes	<input type="checkbox"/> No

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose to the Patent Office all information known to me to be material to patentability as defined in 37 C.F.R. 1.56 which occurred between the filing date of the prior application and the national or PCT international filing date of this application:

<u>PCT/US98/01394</u>	<u>23 January 1998</u>	<u>Pending</u>
(Application Serial No.)	(Filing Date)	(Status)
		(patented, pending, abandoned)
<u>08/819,013</u>	<u>March 17, 1997</u>	<u>Abandoned</u>
(Application Serial No.)	(Filing Date)	(Status)
		(patented, pending, abandoned)
<u>08/788,322</u>	<u>January 24, 1997</u>	<u>Pending</u>
(Application Serial No.)	(Filing Date)	(Status)
		(patented, pending, abandoned)

POWER OF ATTORNEY BY ASSIGNEE

To the Commissioner of Patents and Trademarks:

The undersigned assignee of the entire interest in application for letters patent entitled:
BLNK PROTEINS

and having the named inventors:

Andrew C. Chan and Chong Fu

hereby appoints the following attorneys to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith; said appointment to be to the exclusion of the inventor(s) and his (their) attorney(s) in accordance with the provisions of 37 C.F.R. 1.32: Harold C. Hohbach, Reg. No. 17,757; Aldo J. Test, Reg. No. 18,048; Thomas O. Herbert, Reg. No. 18,612; Donald N. MacIntosh, Reg. No. 20,316; Edward S. Wright, Reg. No. 24,903; David J. Brezner, Reg. No. 24,774; Richard E. Backus, Reg. No. 22,701; James A. Sheridan, Reg. No. 25,435; Robert B. Chickering, Reg. No. 24,286; Richard F. Trecartin, Reg. No. 31,801; Steven F. Caserza, Reg. No. 29,780; Laura L. Kulhanjian, Reg. No. 33,257; Michael A. Kaufman, Reg. No. 32,988; Janet E. Muller, Reg. No. 35,294; Edward N. Bachand, Reg. No. 37,085; R. Michael Ananian, Reg. No. 35,050; Stephen M. Knauer, Reg. No. 38,208; Robin M. Silva, Reg. No. 38,304; David C. Ashby, Reg. No. 36,432; Julian Caplan, Reg. No. 14,785; provided that if any one of said attorneys ceases being affiliated with the law firm of Flehr, Hohbach, Test, Albritton & Herbert as partner, employee or of counsel, such attorney's appointment as attorney and all powers derived therefrom shall terminate on the date such attorney ceases being so affiliated.

In accordance with 37 CFR 3.73 the assignee hereby certifies that the evidentiary documents with respect to its ownership have been reviewed and that, to the best of assignee's knowledge and belief, title is in the assignee seeking to take this action.

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Date:

File No. A-64383-2/RFT/RMS

I hereby appoint, for the benefit of and as agent for the Assignee of this application and to my exclusion if there is now or hereafter such an Assignee: Harold C. Hohbach, Reg. No. 17,757; Aldo J. Test, Reg. No. 18,048; Thomas O. Herbert, Reg. No. 18,612; Donald N. MacIntosh, Reg. No. 20,316; Edward S. Wright, Reg. No. 24,903; David J. Brezner, Reg. No. 24,774; Richard E. Backus, Reg. No. 22,701; James A. Sheridan, Reg. No. 25,435; Robert B. Chickering, Reg. No. 24,286; Richard F. Trecartin, Reg. No. 31,801; Steven F. Caserza, Reg. No. 29,780; Laura L. Kulhanjian, Reg. No. 33,257; Michael A. Kaufman, Reg. No. 32,988; Janet E. Muller, Reg. No. 35,294; Edward N. Bachand, Reg. No. 37,085; R. Michael Ananian, Reg. No. 35,050; Stephen M. Knauer, Reg. No. 38,208; Robin M. Silva, Reg. No. 38,304; David C. Ashby, Reg. No. 36,432; Julian Caplan, Reg. No. 14,785; attorneys and agents with full power of substitution and revocation to prosecute the above-identified application for Letters Patent and to transact all business in the Patent Office connected therewith, provided that if any one of said attorneys ceases being affiliated with the law firm of Flehr Hohbach Test Albritton & Herbert LLP as partner, employee or of counsel, such attorney's appointment as attorney and all powers derived therefrom shall terminate on the date such attorney ceases being so affiliated. .

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File No. A-64383-2/RFT/RMS

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Title 18, United States Code, §1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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Inventor's signature:

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July 22, 1999

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